

GenCore version 5.1.4-P5.4578  
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OM protein - protein search, using sw model

Run on: March 13, 2003, 08:38:46 ; Search time 36 Seconds

(without alignments)  
143.088 Million cell updates/sec

Title: US-09-913-524-9

Perfect score: 143  
Sequence: 1 PWSPALRLQRPPEPSNAHAFCHR 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP-archaea:\*  
2: SP-bacteria:\*  
3: SP-fungi:\*  
4: SP-human:\*  
5: SP-invertebrate:\*  
6: SP-mammal:\*  
7: SP-mmc:\*  
8: SP-organelle:\*  
9: SP-phage:\*  
10: SP-plant:\*  
11: SP-rodent:\*  
12: SP-virus:\*  
13: SP-vertebrate:\*  
14: SP-unclassified:\*  
15: SP-virus:\*  
16: SP-bacteriophage:\*  
17: SP-archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	95.8	366	11 Q8VHP1	Q8VHP1 phodopus su
2	127	88.8	243	6 Q8SPF4	Q8SPF4 sus scrofa
3	94	65.7	329	13 Q9BSU0	Q9BSU0 meleagris g
4	59.5	41.6	116	11 Q9DA10	Q9DA10 mus musculu
5	59	41.3	352	13 Q9DED3	Q9DED3 oncorhynch
6	57	39.9	907	16 Q93JX8	Q93JX8 streptomyce
7	56.5	39.5	135	4 Q8WYG8	Q8WYG8 homo sapien
8	55.5	38.8	1832	2 Q9LRC8	Q9LRC8 polyanium
9	55.5	38.8	1832	2 Q9K1Z8	Q9K1Z8 polyanium
10	54	37.8	320	4 Q9BT76	Q9BT76 homo sapien
11	52.5	36.7	368	4 Q8TAM0	Q8TAM0 homo sapien
12	52	36.4	316	16 Q93JM7	Q93JM7 ralsionia s
13	51	35.7	296	12 Q69118	Q69118 human herpe
14	51	35.7	451	6 Q9GKK5	Q9GKK5 canis fam11
15	51	35.7	458	2 Q9P2A0	Q9P2A0 chromatin
16	51	35.7	615	2 Q93L36	Q93L36 rhizobium 1

17	50.5	35.3	2439	2 Q9LRC5	Q9LRC5 polyanium
18	50.5	35.3	2439	2 Q9K1Z5	Q9K1Z5 polyanium
19	49.5	34.6	420	5 Q9BHX3	Q9BHX3 leishmania
20	49	34.3	46	11 Q8VH23	Q8VH23 mus musculu
21	49	34.3	145	4 Q8WYX9	Q8WYX9 homo sapien
22	49	34.3	223	10 Q9SPE0	Q9SPE0 oryza sativ
23	49	34.3	298	5 Q9676	Q9676 drosophila
24	49	34.3	365	16 Q9KDK7	Q9KDK7 bacillus ba
25	49	34.3	435	5 Q9BL91	Q9BL91 caenorhabdi
26	49	34.3	687	11 Q91XL2	Q91XL2 mus musculu
27	49	34.3	2024	2 Q9EWA3	Q9EWA3 streptomyce
28	48.5	33.9	625	11 Q92315	Q92315 ratius norv
29	48.5	33.9	625	11 Q91Z6	Q91Z6 mus musculu
30	48.5	33.9	671	16 Q9BDY9	Q9BDY9 rhizobium 1
31	48	33.6	83	6 Q93355	Q93355 sus scrofa
32	48	33.6	128	2 Q9XCD3	Q9XCD3 thermomono
33	48	33.6	184	5 Q8SZ05	Q8SZ05 drosophila
34	48	33.6	189	2 Q9R7B5	Q9R7B5 rhodobacter
35	48	33.6	190	2 Q85117	Q85117 rhodobacter
36	48	33.6	349	5 Q9V737	Q9V737 drosophila
37	48	33.6	404	13 Q90Z65	Q90Z65 brachydantio
38	48	33.6	534	4 Q96PK1	Q96PK1 homo sapien
39	48	33.6	536	4 Q9BSA4	Q9BSA4 homo sapien
40	48	33.6	565	2 Q93M23	Q93M23 corynebacte
41	48	33.6	2022	6 Q8WYF8	Q8WYF8 bos taurus
42	47.5	33.2	525	4 Q95392	Q95392 homo sapien
43	47.5	33.2	549	4 Q9H3P2	Q9H3P2 neurospora
44	47.5	33.2	611	3 Q96U07	Q96U07 neurospora
45	47.5	33.2	1469	5 Q9U190	Q9U190 leishmania

## ALIGNMENTS

RESULT 1  
Q8VHP1 PRELIMINARY; PRT; 366 AA.  
ID Q8VHP1  
AC Q8VHP1  
DT 01-MAR-2002 (TrEMBLrel. 20, created)  
DI 01-MAR-2002 (TrEMBLrel. 20, last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)

DE Inhibin alpha-subunit precursor.  
OS Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Phodopus.  
OX NCBI\_Taxid=10044;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY;  
RA Kenny H.A.; Bernard B.J.; Horton T.H.; Moorputt T.K.;  
RT "Photoperiod-dependent Regulation of Inhibin in Siberian Hamsters. I.  
FT Ovarian Inhibin Production and Secretion.";  
RL J. Endocrinol. 0:0-0(2002).  
DR EMBL; AF432351; AAL67332.1;  
DR InterPro: IPR002405; Inhibin\_alpha.  
DR Pfam: PF00019; TGF-beta; 1.  
DR PRINTS: PR00669; INHIBINA.  
DR PRODOM: PD000357; TGFb; 1.  
DR SMART; SM00204; TGFb; 1.  
DR PROSITE; PS00250; TGF-BETA\_1; UNKNOWN.1.  
KW SIGNAL.  
FT SIGNAL  
FT CHAIN  
SQ SEQUENCE 366 AA; 39224 MW; F43DC2DB218B6256 CRC64;

Query Match 95.8%; Score 137; DB 11; Length 366;  
Best Local Similarity 92.0%; Pred. No. 4.2e-11;  
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PWSPALRLQRPPEPSNAHAFCHR 25  
|||||

Db 241 PMSPALRLQRPPEPSAHAFCHR 265

## RESULT 2

Q8SPF4

ID Q8SPF4

PRELIMINARY:

PRT: 243 AA.

AC Q8SPF4

01-JUN-2002 (TREMblrel. 21, Created)

DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Inhibin alpha subunit (Fragment).

GN INHA.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID:9823;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE:95251210; PubMed:7733505;

RA Hiendleder S., Janabek U., Weimann C., Grandke R.,

RT "RFLP markers for the porcine INHA locus.";

RL Anim. Genet. 26:131-132(1995).

RN [2]

RP SEQUENCE FROM N.A.

RA Hiendleder S., Reiner G., Geldermann H., Dzapo V.;

RT "Single nucleotide polymorphisms and PCR-RFLP linkage mapping of the

RL a-inhibin (INHA) gene, a qTL candidate for ovulation rate in swine."

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY028465; AAK3741.1; -

DR EMBL: AY028466; AAK3742.1; -

FT NON\_TER

FT NON\_TER

FT NON\_TER

FT NON\_TER

SQ SEQUENCE

243 AA: 26290 MW; 857E7E245BF7ED57 CRC64;

Query Match

Best Local Similarity 88.8%; Score 127; DB 6; Length 243;

Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PMSPALRLQRPPEPSAHAFCHR 25

129 PMSPALRLQRPPEPSAHAFCHR 153

Db 129 PMSPALRLQRPPEPSAHAFCHR 153

## RESULT 3

Q98S00

ID Q98S00

PRELIMINARY:

PRT: 329 AA.

AC Q98S00

01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Inhibin-alpha.

OS Meleagris gallopavo (Common turkey).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.

OX NCBI\_TaxID:9103;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Ovary;

RA Ahn J., You S., Kim H., Foster D.N., El Halawani M.E.;

RT "Molecular cloning of turkey inhibin-alpha and beta subunits."

RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF363377; AAK21264.1; -

DR HSSP: P18075; IBM.

DR InterPro: IPR002405; Inhibin\_alpha.

DR InterPro: IPR001839; TGF.

DR Pfam: PF00019; TGF-beta; 1.

DR PRINTS: PR00669; INHIBINA.

DR PRODOM: PD000357; TGF; 1.

DR SMART: SM00204; TGF; 1.

DR PROSITE: PS00250; TGF\_BETA\_1; 1.

KM Glycoprotein.

SQ SEQUENCE 329 AA: 35974 MW; E9G1AD113F5FC5C5 CRC64;

## Query Match

Best Local Similarity 65.7%; Score 94; DB 13; Length 329;

Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PMSPALRLQRPPEPSAHAFCHR 25

220 PMSPALRLQRPPEPSAHAFCHR 244

Db 220 PMSPALRLQRPPEPSAHAFCHR 244

## RESULT 4

Q9DAT0

ID Q9DAT0

PRELIMINARY:

PRT: 116 AA.

AC Q9DAT0

01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE 160002914Rix protein.

GN 160002914Rix.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID:10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN:C57BL/6J; TISSUE:PLACENTA;

RA MEDLINE:21085660; PubMed:11217851;

RA Kawai J., Shinagawa A., Shibata K.;

RA Arakawa T., Hara A., Fukunishi Y., Yoshino M., Itoh M., Ishii Y.;

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.;

RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.;

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.;

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.;

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.;

RA Schriml L.M., Strauli F., Suzuki K., Tomita M., Wagner L., Mashio T.;

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli K., Barsh G.;

RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.;

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.;

RA Gustincich S., Hill D., Holman M., Hume D.A., Kamiya M., Lee N.H.;

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.;

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.;

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.;

RA Suzuki H., Toyooka K., Wang K.H., Weiss C., Whitaker C., Wilming L.;

RA Wyszynski-Fortis A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.;

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection."

RI Nature 409:685-690(2001).

DR EMBL: AK005560; BAB24120.1; -

DR MGI: MGI:1917047; 160002914Rix.

SQ SEQUENCE 116 AA: 4629C27654EBC24D CRC64;

Query Match

Best Local Similarity 41.6%; Score 59.5; DB 11; Length 116;

Matches 13; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 SPAALRLQRPPEPSAHAFCHR 25

91 SSAGIX-VTRPEPSAHAFCHR 112

Db 91 SSAGIX-VTRPEPSAHAFCHR 112

## RESULT 5

Q9DED3

ID Q9DED3

PRELIMINARY:

PRT: 352 AA.

AC Q9DED3

01-MAR-2001 (TREMblrel. 16, Created)

DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)

DE 01-JUN-2002 (TREMblrel. 21, Last annotation update)

DE Inhibin.

GN 160002914Rix.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tada T., Bodo M., Hirono I., Takashima F., Aoki T.;  
 RT "Differential expression and cellular localization of actin and  
 RT inhibin mRNA in the rainbow trout ovary and testis";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -; SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: AB044566; BAB19272.1; -;  
 DR InterPro: IPR002405; Inhibin\_alpha.  
 DR InterPro: IPR01839; TGF.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR PRINTS: PR00669; INHIB1A.  
 DR ProDom: PD00037; TGFb; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 KW Glycoprotein.  
 SQ SEQUENCE 352 AA; 39711 MW; ED9CCE860F912ED CRC64;

Query Match 41.38; Score 59; DB 13; Length 352;  
 Best Local Similarity 36.0%; Pred. No. 2.3;  
 Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 PMSPALRLQRPPEPSAHAFCH 25  
 DB 243 PWPSSIDLMPSSQKPEYSIDCR 267

## RESULT 6

Q931X8 PRELIMINARY; PRT; 907 AA.  
 AC Q931X8;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Hypothetical protein SC01292.  
 GN SC01292 OR SCBAC36F5.03.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Saunders D., Harris D.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 KC STRAIN-A3(2);  
 CC Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE:97000351; PubMed-8843436;  
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome";  
 RL Mol. Microbiol. 21:77-96(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2) / M145;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces

RP coelicolor A3(2)";  
 RL Nature 417:141-147(2002).  
 DR EMBL: AL592292; CAC42839.1; -;  
 DR InterPro: IPR001232; SXP1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 907 AA; 66786 MW; D149FDB39C7B53D0 CRC64;

Query Match 39.98; Score 57; DB 16; Length 907;  
 Best Local Similarity 60.0%; Pred. No. 11;  
 Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 PAALRLQRPPEPSAHAFCH 23  
 DB 676 PAALRLQRPVPSDSEWTC 695

## RESULT 7

Q8WYGB PRELIMINARY; PRT; 135 AA.  
 AC Q8WYGB;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Hypothetical 15.1 kDa protein.  
 GN P25933.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gu J.R., Wan D.F., Zhao X.-P., Zhou X.M., Jiang H.-Q., Zhang P.P.,  
 RA Qin W.-X., Huang Y., Qiu X.K., Qian L.F., He L.-P., Li H.N., Yu Y.,  
 RA Yu J., Han L.H.;  
 RT "Novel human cDNA clones with function of inhibiting cancer cell  
 RT growth";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF193049; AAG2477.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 135 AA; 15056 MW; E85C66351D5F6B69 CRC64;

Query Match 39.58; Score 56.5; DB 4; Length 135;  
 Best Local Similarity 47.18; Pred. No. 2;  
 Matches 16; Conservative 3; Mismatches 4; Indels 11; Gaps 3;

QY 1 PMSPALRLQRPPEPSAHAFCH 25  
 DB 6 PMAEA--RLUGRPAPSPATGPKNTAIDASHR 37

## RESULT 8

Q9LBC8 PRELIMINARY; PRT; 1832 AA.  
 AC Q9LBC8;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Polyketide synthase.  
 GN EP0B.  
 OS Polyangium cellulosum.  
 OC Bacteria; Proteobacteria; delta subphylum; Myxobacteria;  
 OC Myxococcales; Sorangineae; Polyangiales; Polyangium.  
 OX NCBI\_TaxID=56;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SO CE90;  
 RX MEDLINE=20130945; PubMed-10662695;  
 RA Molnar I., Schnupp T., Ono M., Zirkle R.E., Milanow M.,  
 RA Novak-Thompson B., Engel N., Toupet C., Strattman A., Cyr D.D.,  
 RA Goelach J., Mayo J.M., Hu A., Goff S., Schmidt J., Ligon J.M.;  
 RT "The biosynthetic gene cluster for the microtubule-stabilizing agents  
 RT epothilones A and B from Sorangium cellulosum So ce90";  
 RL Chem. Biol. 7:97-109(2000).

DR EMBL: AF210843; AAF26920.1; -  
 DR InterPro: IPR001227; Ac\_transferase.  
 DR InterPro: IPR000794; Ketoacyl-synt.  
 DR InterPro: IPR003880; Pantone\_attach.  
 DR Pfam: PF00698; Acyl\_transf\_1.  
 DR Pfam: PF00109; ketoacyl-synt\_1.  
 DR Pfam: PF02801; ketoacyl-synt\_C\_1.  
 DR Pfam: PF00550; pp-binding\_1.  
 DR PROSITE: PS50075; ACP\_DOMAIN; 1.  
 DR PROSITE: PS00606; B\_KETOACYL\_SYNTHASE; 1.  
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN\_1.  
 KW Phosphopantetheine: transferase.  
 SQ SEQUENCE 1832 AA; 193106 MW; B0DBA54B2B57DC91 CRC64;

Query Match 38.8%; Score 55.5; DB 2; Length 1832;  
 Best Local Similarity 48.1%; Pred. No. 34;  
 Matches 13; Conservative 2; Mismatches 5; Indels 7; Gaps 2;

QY 1 PWSF---AALRLQRPPEPSAAHAFCH 24  
 ||| :||||| :||  
 DB 1123 FWPVEVGSRLTLQ---PSCGLMCH 1145

RESULT 9  
 ID Q9K1Z8 PRELIMINARY; PRT; 1832 AA.  
 AC Q9K1Z8.  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE EPOC.  
 GN EPOC.  
 OS Polyangium cellulosum.  
 OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;  
 OC Myxococcales; Sorangineae; Polyangiaceae; Polyangium.  
 OX NCBI\_TaxId=56;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SM44;  
 RX MEDLINE=20293058; PubMed=10831849;  
 RA Julien B., Shah S., Ziermann R., Goldman R., Katz L., Khosla C.;  
 RT "Isolation and characterization of the epoH gene cluster from Sorangium cellulosum."  
 RT cluster from Sorangium cellulosum."  
 RT Gene 249:153-160(2000).  
 RL [2]  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SM44;  
 RX MEDLINE=20115953; PubMed=10649995;  
 RA Tang L., Shah S., Chung L., Carney J., Katz L., Khosla C., Julien B.;  
 RT "Cloning and heterologous expression of the epoH gene cluster."  
 RT Science 287:640-642(2000).  
 RL EMBL: AF217189; AAF62882.1; -  
 DR InterPro: IPR001227; Ac\_transferase.  
 DR InterPro: IPR000794; Ketoacyl-synt.  
 DR InterPro: IPR003880; Pantone\_attach.  
 DR Pfam: PF00698; Acyl\_transf\_1.  
 DR Pfam: PF00109; ketoacyl-synt\_1.  
 DR Pfam: PF02801; ketoacyl-synt\_C\_1.  
 DR Pfam: PF00550; pp-binding\_1.  
 DR PROSITE: PS50075; ACP\_DOMAIN; 1.  
 DR PROSITE: PS00606; B\_KETOACYL\_SYNTHASE; 1.  
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN\_1.  
 KW Phosphopantetheine: transferase.  
 SQ SEQUENCE 1832 AA; 193145 MW; C1EEDB8FA473C2D2 CRC64;

Query Match 38.8%; Score 55.5; DB 2; Length 1832;  
 Best Local Similarity 48.1%; Pred. No. 34;  
 Matches 13; Conservative 2; Mismatches 5; Indels 7; Gaps 2;

QY 1 PWSF---AALRLQRPPEPSAAHAFCH 24  
 ||| :||||| :||  
 DB 1123 FWPVEVGSRLTLQ---PSCGLMCH 1145

RESULT 10  
 ID Q9B176 PRELIMINARY; PRT; 320 AA.  
 AC Q9B176.  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Hypothetical 33.9 kDa protein.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-UTERUS;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/JDNU databases.  
 DR EMBL: BC024304; AA034304.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 320 AA; 33851 MW; 64A6B2E6A8B0EB CRC64;

Query Match 37.8%; Score 54; DB 4; Length 320;  
 Best Local Similarity 41.7%; Pred. No. 10;  
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 PWSFPAALRLQRPPEPSAAHAFCH 24  
 ||| :||||| :||  
 DB 53 PWAAPAPRLGEAPGPTPIVSAH 76

RESULT 11  
 ID Q8TAM0 PRELIMINARY; PRT; 368 AA.  
 AC Q8TAM0.  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE G protein-coupled receptor 62.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/JDNU databases.  
 DR EMBL: BC026357; AA026357.1; -  
 KW Receptor.  
 SQ SEQUENCE 368 AA; 37638 MW; 90506A909812PBA CRC64;

Query Match 36.7%; Score 52.5; DB 4; Length 368;  
 Best Local Similarity 61.1%; Pred. No. 19;  
 Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 WSP-AALRLQRPPEPS 18  
 ||| :||||| :||  
 DB 321 WHPRALQLQRPPECPA 338

RESULT 12  
 ID Q9JUM7 PRELIMINARY; PRT; 316 AA.  
 AC Q9JUM7.  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Regulatory protein (3-COMPARTMENT signal transduction system, component PRR transmembrane protein).  
 DE PRR OR RSP0850 OR RS01621.  
 GN Ralstonia solanacearum (Pseudomonas solanacearum).  
 OS Bacteria; Proteobacteria; delta subdivision; Ralstonia group;

Search completed: March 13, 2003, 12:37:19  
Job time : 36 secs